



SEQUENCE LISTING

<110> Burrell, Michael M.
Cambridge, Amanda P.
Maunders, Martin J.
McQueen-Mason, Simon

<120> Modification of Plant Fibres

<130> 2531-1-001

<140> 09/383,579

<141> 1999-08-25

<150> UK 9818808.9

<151> 1998-08-29

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<170> PatentIn Ver. 2.1

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<211> 488

<212> DNA

<213> Eucalyptus grandis

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tgccctccca acttggccct ctccaaacgac aattgcggct ggtgcaacccc ccctctccag 240
cacttcgata tggccgagcc tgctttctt cagattgccc agtacaaagc tgggattgtc 300
caggtttcct tcagaagggt tccgtgtgt aagaaaggag gggtaagggtt caccatcaat 360
gggcactcct acttcaactt ggtgctgatc accaacgtgg gaggtgctgg tcatgtccat 420
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tgccctccca acttggccct ctccaaacgac aatggcggt ggtgcaacccc ccctctccag 240
cacttcgata tggccgagcc tgctttctt cagattgccc agtacaaagc tgggattgtc 300
caggtttcct tcagaagggt tccgtgtgt aagaaaggag gggtaagggtt caccatcaat 360
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<212> DNA
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<210> 9
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tcacaaacta tttcaaaata taaaacccatt ctt atg gct ttt tct tac tca ccc 174
Met Ala Phe Ser Tyr Ser Pro
1 5

ttc tcc tct ctc ttt ctt cct ttc ttc gtc ttc acc ttc gct 222
Phe Ser Ser Leu Phe Leu Leu Pro Phe Phe Phe Val Phe Thr Phe Ala
10 15 20

gac tac ggt ggc tgg cag agc ggc cac gcc acc ttt tat ggt ggt ggt 270
Asp Tyr Gly Gly Trp Gln Ser Gly His Ala Thr Phe Tyr Gly Gly
25 30 35

gac gca tct ggc acc atg ggt gga gct tgt ggg tat ggg aat tta tac 318
Asp Ala Ser Gly Thr Met Gly Gly Ala Cys Gly Tyr Gly Asn Leu Tyr
40 45 50 55

agc caa ggg tat ggc acg aac acg gtg gcg ctg agc act gcg cta ttt 366
Ser Gln Gly Tyr Gly Thr Asn Thr Val Ala Leu Ser Thr Ala Leu Phe
60 65 70

aac aat gga tta agt tgt ggt gct tgc ttc gaa atg act tgt aca aac 414
Asn Asn Gly Leu Ser Cys Gly Ala Cys Phe Glu Met Thr Cys Thr Asn

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ttt tgc cct cct aac ttt gct ctc cct aac aac aat ggt gga tgg tgc Phe Cys Pro Pro Asn Phe Ala Leu Pro Asn Asn Asn Gly Gly Trp Cys 105 110 115			510
aac cct cct ctc caa cac ttc gac atg gct gag cct gcc ttc ctt caa Asn Pro Pro Leu Gln His Phe Asp Met Ala Glu Pro Ala Phe Leu Gln 120 125 130 135			558
atc gct caa tac cga gct ggt atc gtc ccc gtc tcc ttt cgt agg gta Ile Ala Gln Tyr Arg Ala Gly Ile Val Pro Val Ser Phe Arg Arg Val 140 145 150			606
cca tgt atg aag aaa ggt gga gtg agg ttt aca atc aat ggc cac tca Pro Cys Met Lys Lys Gly Gly Val Arg Phe Thr Ile Asn Gly His Ser 155 160 165			654
tac ttc aac ctc gtt ttg atc aca aac gtc ggt ggc gca ggc gac gtc Tyr Phe Asn Leu Val Leu Ile Thr Asn Val Gly Gly Ala Gly Asp Val 170 175 180			702
cac tct gtg tcg ata aag ggg tct cga act gga tgg caa tcc atg tct His Ser Val Ser Ile Lys Gly Ser Arg Thr Gly Trp Gln Ser Met Ser 185 190 195			750
aga aat tgg ggc caa aac tgg caa agc aac aac tat ctc aat ggc caa Arg Asn Trp Gly Gln Asn Trp Gln Ser Asn Asn Tyr Leu Asn Gly Gln 200 205 210 215			798
ggc ctt tcc ttt caa gtc act ctt agt gat ggt cgc act ctc act gcc Gly Leu Ser Phe Gln Val Thr Leu Ser Asp Gly Arg Thr Leu Thr Ala 220 225 230			846
tat aat ctc gtt cct tcc aat tgg caa ttt ggc caa acc acc tat gaa ggc Tyr Asn Leu Val Pro Ser Asn Trp Gln Phe Gly Gln Thr Tyr Glu Gly 235 240 245			894
cct caa ttc taa accatatcag ccacactgct atgactacta ctacttcaca Pro Gln Phe 250			946
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<210> 10
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 <212> PRT
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 Ala Thr Phe Tyr Gly Gly Asp Ala Ser Gly Thr Met Gly Gly Ala
 35 40 45
 Cys Gly Tyr Gly Asn Leu Tyr Ser Gln Gly Tyr Gly Thr Asn Thr Val
 50 55 60
 Ala Leu Ser Thr Ala Leu Phe Asn Asn Gly Leu Ser Cys Gly Ala Cys
 65 70 75 80
 Phe Glu Met Thr Cys Thr Asn Asp Pro Lys Trp Cys Leu Pro Gly Thr
 85 90 95
 Ile Arg Val Thr Ala Thr Asn Phe Cys Pro Pro Asn Phe Ala Leu Pro

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Pro	Val	Ser	Phe	Arg	Arg	Val	Pro	Cys	Met	Lys	Lys	Gly	Gly	Val	Arg
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	165		170						175						
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	245		250												